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<!--StartFragment-->RESULT 2
PSPTXAG
LOCUS      PSPTXAG                      3234 bp    DNA        linear    PLN 18-APR-2005
DEFINITION Pisum sativum ptxA gene.
ACCESSION  X67427
VERSION    X67427.1  GI:2578443
KEYWORDS   ptxA gene.
SOURCE     Pisum sativum (pea)
ORGANISM   Pisum sativum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae;
            Pisum.
REFERENCE  1
AUTHORS    Bown,D.P.
JOURNAL    Thesis (1992) Department of Biological Sciences, University of
            Durham, Durham, U.K
REFERENCE  2  (bases 1 to 3234)
AUTHORS    Bown,D.P.
TITLE      Direct Submission
JOURNAL    Submitted (02-JUN-1992) D.P. Bown, University of Durham, Dept. of
            Biological Sciences, Science Site, South Rd, Durham, DH1 3LE, UK
FEATURES   Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.7e-244;
Matches 863; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GCAATTTTTGTGAAGCTGAGGAGGATTGGATTTTACACCTATTCAAAAGTCATTCAAA 60
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Db      81  GCAATTTTTGTGAAGCTGAGGAGGATTGGATTTTACACCTATTCAAAAGTCATTCAAA 140

Qy      61  GTTTGTCCTCCATTCAAGGATGAATGTAGATTTTTCAAGCATCAACACAAGATCACT 120
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Db      141  GTTTGTCCCTCCATTCAAGGATGAATGTAGATTTTTCAAGCATCAAACACAAGAATCACT  200
Qy      121  AGCATAACATGCTTTGAAACCCACACACTTAAATTAATGTTAGGAATATCAAATCCAATA  180
      |||
Db      201  AGCATAACATGCTTTGAAACCCACACACTTAAATTAATGTTAGGAATATCAAATCCAATA  260
Qy      181  TAAATCATAGTTGTCAATTACATACTCAATCAAGTCCCTTTCTTTTACCCAATAAACAT  240
      |||
Db      261  TAAATCATAGTTGTCAATTACATACTCAATCAAGTCCCTTTCTTTTACCCAATAAACAT  320
Qy      241  CAACATATTGCTTCTTCCATTAAAGCATATAAACATCAAAGTCTAAAAC TAGCAAAATGTT  300
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Db      321  CAACATATTGCTTCTTCCATTAAAGCATATAAACATCAAAGTCTAAAAC TAGCAAAATGTT  380
Qy      301  GTTTTTAGGATGACACATTTCATACATAGTTTAAAGATACTTGATTCGATTACAAAAAG  360
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Qy      781  ATAAACCTCATCACTCATTCATTTTTTTTAAAGTGCAAAGCTTCATAGTAGTGAGCACACA  840
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Db      861  ATAAACCTCATCACTCATTCATTTTTTTTAAAGTGCAAAGCTTCATAGTAGTGAGCACACA  920
Qy      841  CATTACACTAAAAATCTTCGAAAC  863
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